



39780-1216R1D4 saved November 17 2005.TXT

SEQUENCE LISTING

<110> Ashkenazi, Avi J.
Fong, Sherman
Goddard, Audrey
Gurney, Austin L.
Napier, Mary A.
Tumas, Daniel
Wood, William I.

<120> COMPOUNDS, COMPOSITIONS AND METHODS FOR
THE TREATMENT OF DISEASES CHARACTERIZED BY A33- RELATED
ANTIGENS

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<140> 10/785,220
<141> 2004-02-24

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<151> 1999-03-05

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<151> 1998-11-20

<150> US 60/066,364
<151> 1997-11-21

<150> US 60/078,936
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<151> 1998-09-17

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Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe
50 55 60
Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr
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Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe
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Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser
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Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val
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Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr
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Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn
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Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro
180 185 190
Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly
195 200 205
Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser
210 215 220
Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val
225 230 235 240
Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly
245 250 255
Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly
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<212> PRT

<213> Homo sapiens

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35 40 45
Tyr Thr Gln Val Leu Val Lys Trp Leu Val Gln Arg Gly Ser Asp Pro
50 55 60
Val Thr Ile Phe Leu Arg Asp Ser Ser Gly Asp His Ile Gln Gln Ala
65 70 75 80
Lys Tyr Gln Gly Arg Leu His Val Ser His Lys Val Pro Gly Asp Val
85 90 95
Ser Leu Gln Leu Ser Thr Leu Glu Met Asp Asp Arg Ser His Tyr Thr
100 105 110
Cys Glu Val Thr Trp Gln Thr Pro Asp Gly Asn Gln Val Val Arg Asp
115 120 125
Lys Ile Thr Glu Leu Arg Val Gln Lys Leu Ser Val Ser Lys Pro Thr
130 135 140
Val Thr Thr Gly Ser Gly Tyr Gly Phe Thr Val Pro Gln Gly Met Arg
145 150 155 160
Ile Ser Leu Gln Cys Gln Ala Arg Gly Ser Pro Pro Ile Ser Tyr Ile
165 170 175
Trp Tyr Lys Gln Gln Thr Asn Asn Gln Glu Pro Ile Lys Val Ala Thr
180 185 190
Leu Ser Thr Leu Leu Phe Lys Pro Ala Val Ile Ala Asp Ser Gly Ser
195 200 205
Tyr Phe Cys Thr Ala Lys Gly Gln Val Gly Ser Glu Gln His Ser Asp
210 215 220
Ile Val Lys Phe Val Val Lys Asp Ser Ser Lys Leu Leu Lys Thr Lys
225 230 235 240
Thr Glu Ala Pro Thr Thr Met Thr Tyr Pro Leu Lys Ala Thr Ser Thr
245 250 255
Val Lys Gln Ser Trp Asp Trp Thr Thr Asp Met Asp Gly Tyr Leu Gly
260 265 270
Glu Thr Ser Ala Gly Pro Gly Lys Ser Leu Pro Val Phe Ala Ile Ile

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275 280 285
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gcttgcctt ccatccaagc ctacagttaa catcccccc tctgcccacca ttgggaaccg 180
ggcagtgcgt acatgctcag aacaagatgg ttccccacct tctgaataca cctggttcaa 240
agatggata gtgatgccta cgaatcccaa aagcaccctg gccttcagca actcttccta 300
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ccaactggta tcaccttcaa gtccgtgaca cggaaagaca ctgggacata cacttgtatg 420
gtctctgagg aaggcggcaa cagctatggg gaggtcaagg tcaagctcat cgtgctgtg 480
cctccatcca agcctacagt taacatcccc tcctctggca ccattggaa ccgggcagtg 540
ctgacatgct cagaacaaga tggttccca cttctgtaa acacctgggt caaagatggg 600
atagtgtatgc ctacgaatcc caaaaggcacc cgtgccttca gcaactcttc ctatgtcctg 660
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gactcctgat ggcaacccaag tcgtgagaga taagattact gagctccgtg tccagaaact 180
ctctgtctcc aagcccacag tgacaactgg cagcggttat ggcttcacgg tgccccaggg 240
aatgaggatt agccttcaat gccagggttc ggggtctcc tcccatcagt tatatttgg 300

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ggCTCTGAGC AGCACAGCGA CATTGTAAG tttGTGGTCA aAGACTCCTC AAAGCTACTC 480
aAGACCAAGA CTGAGGCACC TACAACCATG ACATACCCCT TGAAAGCAAC ATCTACAGTG 540
aAGCAGTCCT GGGACTGGAC CACTGACATG GATGGCTACCG TTGGAGAGAC CAGTGCTGGG 600
ccAGGAAAGA GCCTGCCTG CTTGCCATC ATCCTCATCA TCTCCTTGTG CTGTATGGTG 660
gtTTTACCA TGGCCTATAT CATGCTCTGT CGGAAGACAT CCCAACAAAGA GCACTGCTAC 720
gaAGCAGCCA GGGCACATGC CAGAGGGCC AACGACTCTG GAGAAACCAT GAGGGTGGCC 780
atCTTCGCAA GTGGCTGCTC CAGTGATGAG CCAACTTCCC AGAATCTGGG GCAACAACTA 840
ctCTGATGAG CCCTGCTAG GACAGGAGTA CCAGATCATC GCCCAGATCA ATGGCAACTA 900
cgCCCCCTG CTGGACACAG TTCCTCTGGA TTATGAGTT CTGCCACTG AGGGCAAAAG 960
tgtCTGTTAA AATGCCCCA TTAGGCCAGG ATCTGCTAC ATCTCTTCC GATAGGCCA AAGTGTCCGC 1020
tgcCTCTGC ATGGCCTTC TCCCTGCTAC CTCTCTTCC GATAGGCCA AAGTGTCCGC 1080
ctACCAACAC TGGAGCCGCT GGGAGTCACT GGCTTGGCC TGGAAATTG CAGATGCATC 1140
tcaAGTAAGC CAGCTGCTG ATTGGCTCT GGGCCCTTCT AGTATCTCTG CCGGGGGCTT 1200
ctGGTACTCC TCTCTAAATA CCAGAGGGAA GATGCCATA GCACTAGGAC TTGGTCATCA 1260
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<210> 6

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<212> PRT

<213> Homo sapiens

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35 40 45
Thr Ser Ser Arg Glu Gly Leu Ile Gln Trp Asp Lys Leu Leu Leu Thr
50 55 60
His Thr Glu Arg Val Val Ile Trp Pro Phe Ser Asn Lys Asn Tyr Ile
65 70 75 80
His Gly Glu Leu Tyr Lys Asn Arg Val Ser Ile Ser Asn Asn Ala Glu
85 90 95
Gln Ser Asp Ala Ser Ile Thr Ile Asp Gln Leu Thr Met Ala Asp Asn
100 105 110
Gly Thr Tyr Glu Cys Ser Val Ser Leu Met Ser Asp Leu Glu Gly Asn
115 120 125
Thr Lys Ser Arg Val Arg Leu Leu Val Leu Val Pro Pro Ser Lys Pro
130 135 140
Glu Cys Gly Ile Glu Gly Glu Thr Ile Ile Gly Asn Asn Ile Gln Leu
145 150 155 160
Thr Cys Gln Ser Lys Glu Gly Ser Pro Thr Pro Gln Tyr Ser Trp Lys
165 170 175
Arg Tyr Asn Ile Leu Asn Gln Glu Gln Pro Leu Ala Gln Pro Ala Ser
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Gly Gln Pro Val Ser Leu Lys Asn Ile Ser Thr Asp Thr Ser Gly Tyr
195 200 205
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210 215 220
Thr Val Ala Val Arg Ser Pro Ser Met Asn Val Ala Leu Tyr Val Gly
225 230 235 240
Ile Ala Val Gly Val Val Ala Ala Leu Ile Ile Ile Gly Ile Ile Ile
245 250 255
Tyr Cys Cys Cys Arg Gly Lys Asp Asp Asn Thr Glu Asp Lys Glu
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<211> 2181
<212> DNA
<213> *Homo sapiens*

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| ggggatctta | ctgggcctgc | tactccctggg | gcacctaaca | gtggacactt | atggccgtcc | 180 | |
| catcctggaa | gtgccagaga | gtgtAACAGG | accttggaaa | ggggatgtga | atcttccctg | 240 | |
| cacccatgac | cccctgcaag | gctacaccca | agtcttgggt | aagtggctgg | tacaacgtgg | 300 | |
| ctcagaccct | gtcaccatct | ttctacgtga | ctcttctgga | gaccatatcc | agcaggcaaa | 360 | |
| gtaccaggc | cgccctgcatg | tgagccacaa | gttccagga | gatgtatccc | tccaattttag | 420 | |
| caccctggag | atggatgacc | ggagccacta | cacgtgtgaa | gtcacctggc | agactccctg | 480 | |
| tggcaaccaa | gtcgtgagag | ataagattac | ttagctccgt | gtccagaaac | tctctgtctc | 540 | |
| caagccccaca | gtgacaacty | gcagccgtta | tggcttcacg | gtgccccagg | gaatgaggat | 600 | |
| tagccttca | tgcaggcgtc | ggggctctcc | tcccatca | tatatttgg | ataagcaaca | 660 | |
| gactaataac | caggaaccca | tcaaagtgc | aacccta | accttactt | tcaagccctg | 720 | |
| ggtgatagcc | gactcaggct | cctatttctg | cactgcca | ggccagggtt | gctctgagca | 780 | |
| gcacagcgc | attgtgaagt | ttgtgttca | agactcctca | aagctactca | agaccaagac | 840 | |
| tgaggcacct | acaaccatga | cataccctt | gaaagcaaca | tctacagtga | agcagtccctg | 900 | |
| ggactggacc | actgacatgg | atggctacct | tggagagacc | agtgtggc | caggaaagag | 960 | |
| cctgcctgtc | tttgcacatca | tcctcatcat | tccttgc | tgtatgggg | tttttaccat | 1020 | |
| ggcctatatac | atgctctgtc | ggaagacatc | ccaacaagag | catgtctacg | aagcagccag | 1080 | |
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| agggtcagga | catagctgcc | ttccctctct | caggcacctt | ctgaggttgt | tttggccctc | 1260 | |
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| ccaagtcct | tcttatgggt | ggtggctct | ttggccatag | ggcacatgcc | agagaggcca | 1440 | |
| acgactctgg | agaaaaccatg | agggtggcca | tcttcgc | tggctgtcc | agtgtatgagc | 1500 | |
| caactccca | gaatctgggc | aacaactact | ctgatgagcc | ctgcatagga | caggagtacc | 1560 | |
| agatcatcgc | ccagatcaat | ggcaactacg | cccgccctgt | ggacacagtt | cctctggatt | 1620 | |
| atgagtttct | ggccactgag | ggcaaaagtg | tctgttaaaa | atgccccatt | aggccaggat | 1680 | |
| ctgctgacat | aattgcctag | tcagttcttg | ccttctgc | ggcccttctc | cctgtctact | 1740 | |
| ctttccctgg | atagccaaa | gtgtccgc | accaacactg | gagccgtgg | gagtcactgg | 1800 | |
| ctttccctgg | gaatttgc | gatgcac | aagtaagcc | gctgtggat | ttggctctgg | 1860 | |
| gccccctttag | tatctctgcc | gggggttct | gttactcc | tctaaatacc | agagggaaaga | 1920 | |
| tgccccatagc | actaggactt | ggtcatcatg | cctacagaca | ctattcaact | ttggcatctt | 1980 | |
| gccaccagaa | gaccggaggg | aggctcagct | ctgcccagctc | agaggaccag | ctatattccag | 2040 | |
| gatcatttct | ctttcttgc | ggccagacag | cttttaattt | aaattgttat | ttcacagggcc | 2100 | |
| agggttcagt | tctgctctc | cactataatg | ctaatgttct | gactctctcc | ttggtgctcaa | 2160 | |
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<212> DNA
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<210> 9

<211> 312

<212> PRT

<213> Homo sapiens

<400> 9

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35 40 45
Ala Cys Lys Thr Pro Lys Lys Thr Val Ser Ser Arg Leu Glu Trp Lys
50 55 60
Lys Leu Gly Arg Ser Val Ser Phe Val Tyr Tyr Gln Gln Thr Leu Gln
65 70 75 80
Gly Asp Phe Lys Asn Arg Ala Glu Met Ile Asp Phe Asn Ile Arg Ile
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Ala Pro Ser Glu Gln Gly Gln Asn Leu Glu Glu Asp Thr Val Thr Leu
115 120 125
Glu Val Leu Val Ala Pro Ala Val Pro Ser Cys Glu Val Pro Ser Ser
130 135 140
Ala Leu Ser Gly Thr Val Val Glu Leu Arg Cys Gln Asp Lys Glu Gly
145 150 155 160
Asn Pro Ala Pro Glu Tyr Thr Trp Phe Lys Asp Gly Ile Arg Leu Leu
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Glu Asn Pro Arg Leu Gly Ser Gln Ser Thr Asn Ser Ser Tyr Thr Met
180 185 190
Asn Thr Lys Thr Gly Thr Leu Gln Phe Asn Thr Val Ser Lys Leu Asp
195 200 205
Thr Gly Glu Tyr Ser Cys Glu Ala Arg Asn Ser Val Gly Tyr Arg Arg
210 215 220
Cys Pro Gly Lys Arg Met Gln Val Asp Asp Leu Asn Ile Ser Gly Ile
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Ile Ala Ala Val Val Val Val Ala Leu Val Ile Ser Val Cys Gly Leu
245 250 255
Gly Val Cys Tyr Ala Gln Arg Lys Gly Tyr Phe Ser Lys Glu Thr Ser
260 265 270
Phe Gln Lys Ser Asn Ser Ser Lys Ala Thr Thr Met Ser Glu Asn
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<211> 300
<212> PRT
<213> Mus musculus

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35 40 45
Cys Thr Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe Val
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Pro Tyr Ala Asp Arg Val Thr Phe Ser Ser Ser Gly Ile Thr Phe Ser
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Ser Val Thr Arg Lys Asp Asn Gly Glu Tyr Thr Cys Met Val Ser Glu
100 105 110
Glu Gly Gln Asn Tyr Gly Glu Val Ser Ile His Leu Thr Val Leu
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130 135 140
Gly Asn Arg Ala Val Leu Thr Cys Ser Glu His Asp Gly Ser Pro Pro
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Ser Glu Tyr Ser Trp Phe Lys Asp Gly Ile Ser Met Leu Thr Ala Asp
165 170 175
Ala Lys Lys Thr Arg Ala Phe Met Asn Ser Ser Phe Thr Ile Asp Pro
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Lys Ser Gly Asp Leu Ile Phe Asp Pro Val Thr Ala Phe Asp Ser Gly
195 200 205
Glu Tyr Tyr Cys Gln Ala Gln Asn Gly Tyr Gly Thr Ala Met Arg Ser
210 215 220
Glu Ala Ala His Met Asp Ala Val Glu Leu Asn Val Gly Gly Ile Val
225 230 235 240
Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Leu Leu Ile Phe Gly
245 250 255
Val Trp Phe Ala Tyr Ser Arg Gly Tyr Phe Glu Thr Thr Lys Lys Gly
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<212> DNA
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ctctggccctg tcctcctgaa tacaagctga ctgacattga ctgtgtctgt ggaaaatggg 1560
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accgctgctc taaagaaaaag aaaactggag gctgggcgca gtggctcacg cctgtaatcc 1680
cagaggctga ggcaggcggc tcacctgagg tcggggatcc gggatcagcc tgaccaacat 1740
ggagaaaccc tactggaaat acaaagttt ccaggcatgg tgggtcatgc ctgtagtccc 1800
agctgctcag gagcctggca acaagagcaa aactccagct ca 1842

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<220>

<223> Synthetic Oligonucleotide Primer

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24

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<211> 50

<212> DNA

<213> Artificial Sequence

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<223> Synthetic Oligonucleotide Hybridization Probe

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50

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<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Primer

<400> 14

acacctgggtt caaagatggg

20

<210> 15

<211> 24

<212> DNA

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<220>

<223> Synthetic Oligonucleotide Primer

<400> 15
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<400> 18
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 <213> Homo sapiens

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 Ser Ser Pro Arg Val Glu Trp Lys Phe Asp Gln Gly Asp Thr Thr Arg
 35 40 45
 Leu Val Cys Tyr Asn Asn Lys Ile Thr Ala Ser Tyr Glu Asp Arg Val
 50 55 60
 Thr Phe Leu Pro Thr Gly Ile Thr Phe Lys Ser Val Thr Arg Glu Asp
 65 70 75 80
 Thr Gly Thr Tyr Thr Cys Met Val Ser Glu Glu Gly Gly Asn Ser Tyr
 85 90 95
 Gly Glu Val Lys Val Lys Leu Ile Val Leu Val Pro Pro Ser Lys Pro
 100 105 110
 Thr Val Asn Ile Pro Ser Ser Ala Thr Ile Gly Asn Arg Ala Val Leu
 115 120 125
 Thr Cys Ser Glu Gln Asp Gly Ser Pro Pro Ser Glu Tyr Thr Trp Phe
 130 135 140
 Lys Asp Gly Ile Val Met Pro Thr Asn Pro Lys Ser Thr Arg Ala Phe
 145 150 155 160
 Ser Asn Ser Ser Tyr Val Leu Asn Pro Thr Thr Gly Glu Leu Val Phe
 165 170 175
 Asp Pro Leu Ser Ala Ser Asp Thr Gly Glu Tyr Ser Cys Glu Ala Arg
 180 185 190
 Asn Gly Tyr Gly Thr Pro Met Thr Ser Asn Ala Val Arg Met Glu Ala
 195 200 205
 Val Glu Arg Asn Val Gly Val Ile Val Ala Ala Val Leu Val Thr Leu
 210 215 220
 Ile Leu Leu Gly Ile Leu Val Phe Gly Ile Trp Phe Ala Tyr Ser Arg
 225 230 235 240
 Gly His Phe Asp Arg Thr Lys Lys Gly Thr Ser Ser Lys Lys Val Ile
 245 250 255
 Tyr Ser Gln Pro
 260

<210> 24
 <211> 270
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<213> Homo sapiens

<400> 24

Val Arg Val Thr Val Asp Ala Ile Ser Val Glu Thr Pro Gln Asp Val
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 35 40 45
 Leu Thr His Thr Glu Arg Val Val Ile Trp Pro Phe Ser Asn Lys Asn
 50 55 60
 Tyr Ile His Gly Glu Leu Tyr Lys Asn Arg Val Ser Ile Ser Asn Asn
 65 70 75 80
 Ala Glu Gln Ser Asp Ala Ser Ile Thr Ile Asp Gln Leu Thr Met Ala
 85 90 95
 Asp Asn Gly Thr Tyr Glu Cys Ser Val Ser Leu Met Ser Asp Leu Glu
 100 105 110
 Gly Asn Thr Lys Ser Arg Val Arg Leu Leu Val Leu Val Pro Pro Ser
 115 120 125
 Lys Pro Glu Cys Gly Ile Glu Gly Glu Thr Ile Ile Gly Asn Asn Ile
 130 135 140
 Gln Leu Thr Cys Gln Ser Lys Glu Gly Ser Pro Thr Pro Gln Tyr Ser
 145 150 155 160
 Trp Lys Arg Tyr Asn Ile Leu Asn Gln Glu Gln Pro Leu Ala Gln Pro
 165 170 175
 Ala Ser Gly Gln Pro Val Ser Leu Lys Asn Ile Ser Thr Asp Thr Ser
 180 185 190
 Gly Tyr Tyr Ile Cys Thr Ser Ser Asn Glu Glu Gly Thr Gln Phe Cys
 195 200 205
 Asn Ile Thr Val Ala Val Arg Ser Pro Ser Met Asn Val Ala Leu Tyr
 210 215 220
 Val Gly Ile Ala Val Gly Val Val Ala Ala Leu Ile Ile Ile Gly Ile
 225 230 235 240
 Ile Ile Tyr Cys Cys Cys Arg Gly Lys Asp Asp Asn Thr Glu Asp
 245 250 255
 Lys Glu Asp Ala Arg Pro Asn Arg Glu Ala Tyr Glu Glu Pro
 260 265 270

<210> 25

<211> 263

<212> PRT

<213> Homo sapiens

<400> 25

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 20 25 30
 Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe Asp Gln Gly Asp
 35 40 45
 Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr Ala Ser Tyr Glu
 50 55 60
 Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe Lys Ser Val Thr
 65 70 75 80
 Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser Glu Glu Gly Gly
 85 90 95
 Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val Leu Val Pro Pro
 100 105 110
 Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr Ile Gly Asn Arg
 115 120 125
 Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro Pro Ser Glu Tyr
 130 135 140

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Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn Pro Lys Ser Thr
145 150 155 160
Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro Thr Thr Gly Glu
165 170 175
Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly Glu Tyr Ser Cys
180 185 190
Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser Asn Ala Val Arg
195 200 205
Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val Ala Ala Val Leu
210 215 220
Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly Ile Trp Phe Ala
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Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly Thr Ser Ser Lys
245 250 255
Lys Val Ile Tyr Ser Gln Pro
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<210> 26

<211> 273

<212> PRT

<213> Homo sapiens

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20 25 30
Thr Tyr His Thr Ser Thr Ser Arg Glu Gly Leu Ile Gln Trp Asp
35 40 45
Lys Leu Leu Leu Thr His Thr Glu Arg Val Val Ile Trp Pro Phe Ser
50 55 60
Asn Lys Asn Tyr Ile His Gly Glu Leu Tyr Lys Asn Arg Val Ser Ile
65 70 75 80
Ser Asn Asn Ala Glu Gln Ser Asp Ala Ser Ile Thr Ile Asp Gln Leu
85 90 95
Thr Met Ala Asp Asn Gly Thr Tyr Glu Cys Ser Val Ser Leu Met Ser
100 105 110
Asp Leu Glu Gly Asn Thr Lys Ser Arg Val Arg Leu Leu Val Leu Val
115 120 125
Pro Pro Ser Lys Pro Glu Cys Gly Ile Glu Gly Glu Thr Ile Ile Gly
130 135 140
Asn Asn Ile Gln Leu Thr Cys Gln Ser Lys Glu Gly Ser Pro Thr Pro
145 150 155 160
Gln Tyr Ser Trp Lys Arg Tyr Asn Ile Leu Asn Gln Glu Gln Pro Leu
165 170 175
Ala Gln Pro Ala Ser Gly Gln Pro Val Ser Leu Lys Asn Ile Ser Thr
180 185 190
Asp Thr Ser Gly Tyr Tyr Ile Cys Thr Ser Ser Asn Glu Glu Gly Thr
195 200 205
Gln Phe Cys Asn Ile Thr Val Ala Val Arg Ser Pro Ser Met Asn Val
210 215 220
Ala Leu Tyr Val Gly Ile Ala Val Gly Val Val Ala Ala Leu Ile Ile
225 230 235 240
Ile Gly Ile Ile Ile Tyr Cys Cys Cys Cys Arg Gly Lys Asp Asp Asn
245 250 255
Thr Glu Asp Lys Glu Asp Ala Arg Pro Asn Arg Glu Ala Tyr Glu Glu
260 265 270
Pro

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atcatgtgaa gtaccctctt ctgctctgag tggaaactgtg gtagagctac gatgtcaaga 180
caaagaaggg aatccagctc ctgaatacac atggtttaag gatggcatcc gtttgctaga 240
aaatcccaga cttggctccc aaagcaccaa cagctcatac acaatgaata caaaaactgg 300
aactctgcaa ttaataactg tttccaaact ggacactgga gaatattcct gtgaagcccg 360
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<210> 28

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Primer

<400> 28

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<210> 29

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Primer

<400> 29

acctgcgata tccaacagaa ttg 23

<210> 30

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Hybridization Probe

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